

Fig. 1.

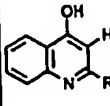
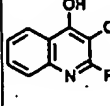
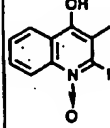
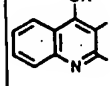
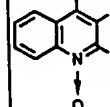
	M+H ions	R =
	Series A	
	216	C ₅ H ₁₁
	230	C ₆ H ₁₃
	244	C ₇ H ₁₅ HQ
	258	C ₈ H ₁₇
	272	C ₉ H ₁₉ HNQ
	300	C ₁₁ H ₂₃
	Series B	
	232	C ₅ H ₁₁
	246	C ₆ H ₁₃
	260	C ₇ H ₁₅ PQS
	274	C ₈ H ₁₇
	288	C ₉ H ₁₉
	316	C ₁₁ H ₂₃
	Series C	
	232	C ₅ H ₁₁
	246	C ₆ H ₁₃
	260	C ₇ H ₁₅ HQNO
	274	C ₈ H ₁₇
	288	C ₉ H ₁₉
	316	C ₁₁ H ₂₃
	Series D	
	270	C ₉ H ₁₇
	298	C ₁₁ H ₂₁
	Series E	
	258	C ₇ H ₁₃
	272	C ₈ H ₁₅
	286	C ₉ H ₁₇
	314	C ₁₁ H ₂₁

Fig. 2.

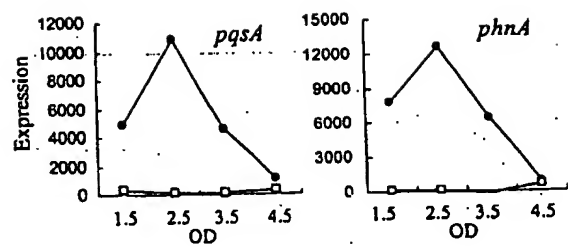


Fig. 3

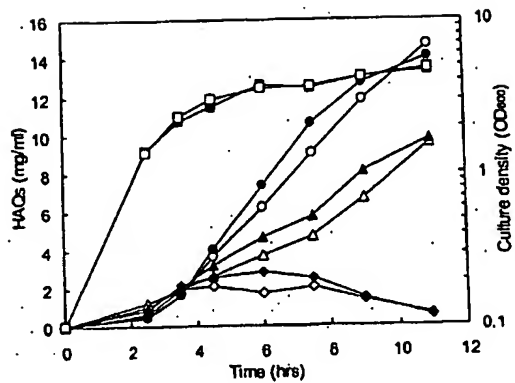


Fig. 4.

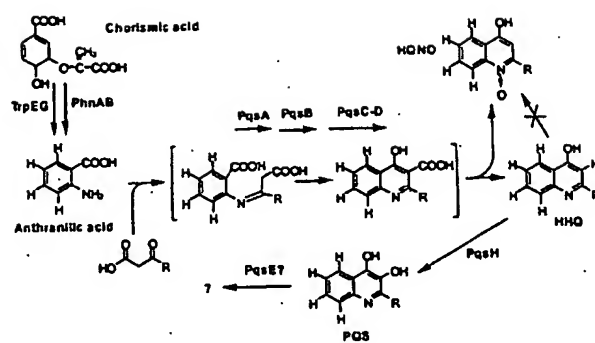


Fig. 5.

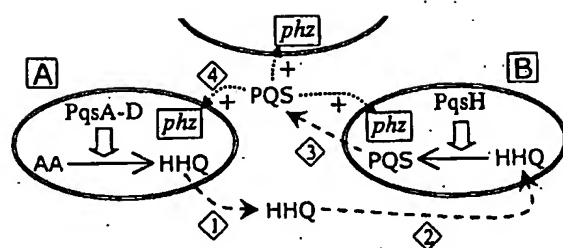


Fig. 6.

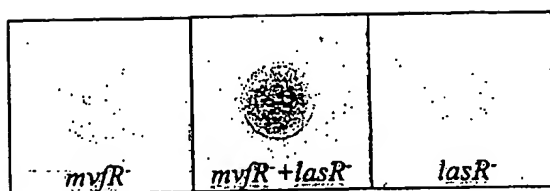


Fig. 7.

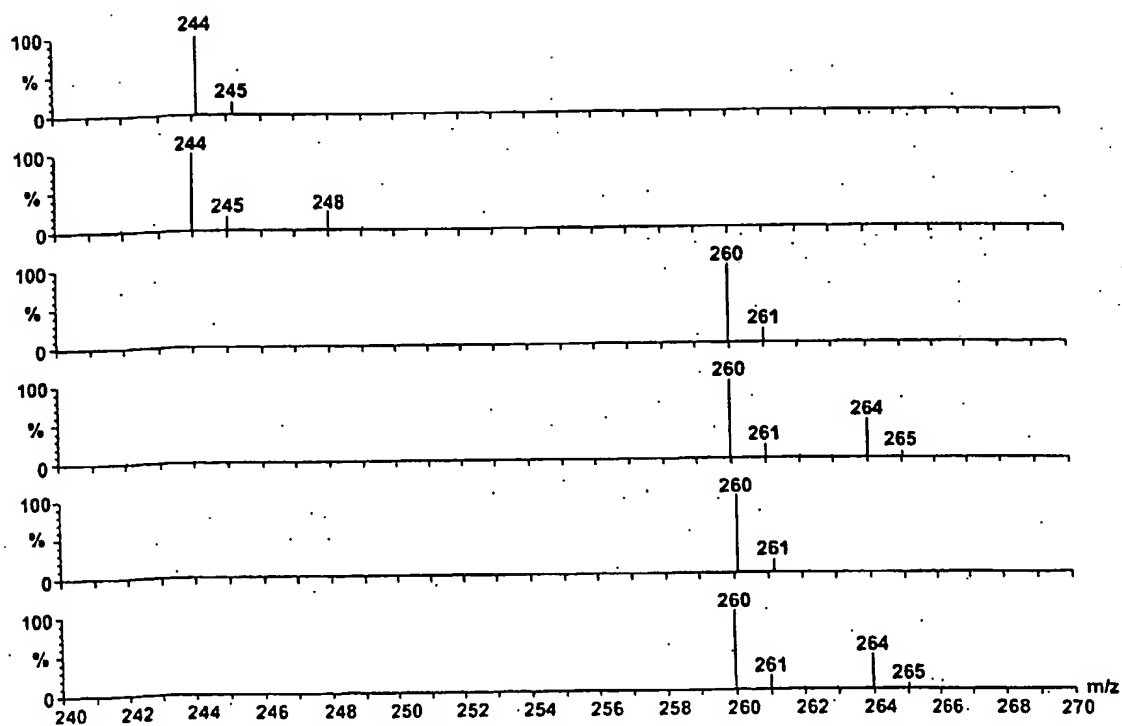


Fig. 8.

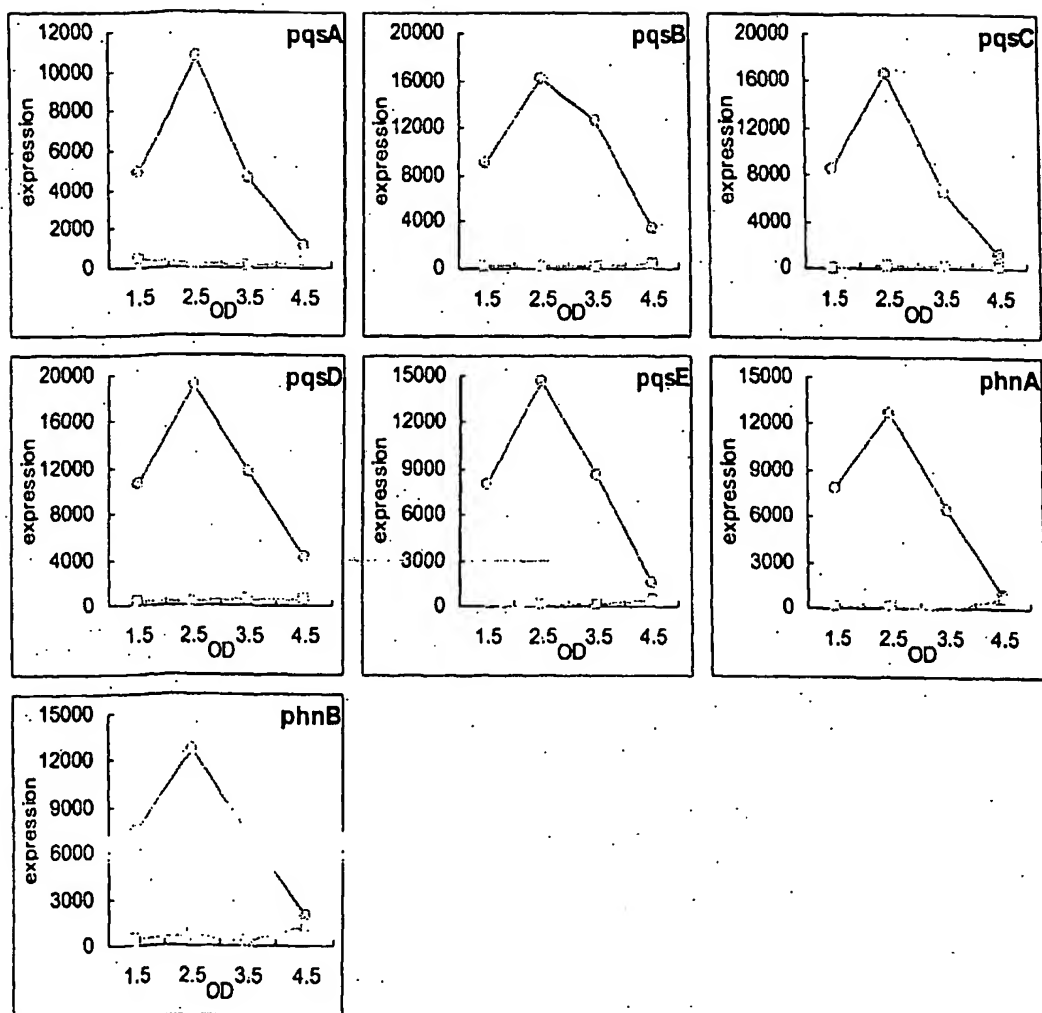


Fig. 9.

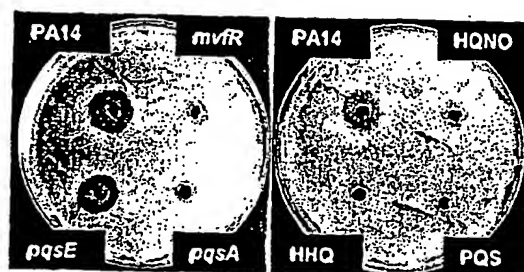


Fig. 10.

All sequences are from *Pseudomonas aeruginosa*

pqsA (SEQ ID NO:1)

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CACCGGCGACCTGTTTCGAGCGCGACGAGTCGGGTGCCTACCGTCACTGTGGGCGGGAAGACGATCTGTTCA
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pqsB (SEQ ID NO:2)

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pqsC (SEQ ID NO:3)

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CCGGAACCCGACCGCGAGGCCAAGCCGGGCTTTATTTCTCGTTGTTTCAGCGACGGCCAGAACAAAGAT

Figure 11

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GGCCAGCTTCGTTCCGACCAACGTGCCGATCGCGATGCGCCGGGCGTTGGAAAAGGCCGGCCTGGGCAGCG
ATGACATCGATTATTTTCGTCTTCCACCAGCCAGCGCCGTTCTGGTCAAGGCCTGGGCCGAGGGCATCGGT
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***pqsD* (SEQ ID NO:4)**

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***pqsE* (SEQ ID NO:5)**

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***pqsH* (SEQ ID NO:6)**

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ACGACCTCGAGGAGTTGGCCGGCGCCTCCTGGTGCCGCGGACGGGTAGTGCTGATCGGTGACGCCGACAC

Figure 11

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GCCATGACGCCGAACCTGGGGCAGGGCGCGGCCATGGCCCTGGAGGACGCCTTCCTGCTGGCGCGCCTGTG
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GGCCGCACAGTAG

***pqsL* (SEQ ID NO:7)**

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CGGGTCCGCCATGAGCTGGAGGTCTATCACGACGGCGAGCTGCTTCGCTATTTCAACTATTCCAGCGTCGA
CGCGCGCGGCTATTTTCATCCTCATGCCCTGCGAGTCGCTGCGCCGCTGGTACTGGAAAAAATCGACGGCG
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ACCAGCCTGGAGGATCGCCAGCGCTTCGCCGGGGTCTTCGACACCGCCCTGCAGGGCAGCAGCCGTACGCC
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PGLSPGYWRASEEQARFAGGWYRTGDLFERDESGAYRHCGRDDLFKVNWRVWVPTQVEQAICRHLPEVS
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***PqsB* (SEQ ID NO:9)**

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***PqsC* (SEQ ID NO:10)**

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PqsD (SEQ ID NO:11)

MGNPILAGLGFSLPKRQVSNHDLVGRINTSDEFIVERTGVRTRYHVEPEQAVSALMVPAARQAIEAAGLLP
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 LSKRMDCSRGRNLSILLGDGAGAVVVSAGESLEDGLLDLRLGADGNYFDLLMTAAPGSASPTFLDENVLR
 EGGGEFLMRGRPMFEHASQTLVRIAGEMLAAHELTLDIDHVIHQPNLRILDAVQEQLGIPQHKFAVTVD
 RLGNMASASTPVTLAMFWPDIQPGQRVLVLTYGSGATWGAALYRKPEEVNRP

PqsE (SEQ ID NO:12)

MLRLSAPQLDDDLCLLDVQVPVFLRLGEASWALVEGGISRDAELVWADLCRWVADPSQVHYWLITHKH
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 LELGPRHRLQVIEAHGHSDDHVVFYDVRRLRLFCGDALGEFDEAEGVWRPLVFDDMEAYLESRLRLPT
 LLQLIPGHGGLLRGLAADGAESAYTECLRLCRLLLRQSMGESLDELSEELHRAWGGQSVDFLPGLHLG
 SMRRMLEILSRQALPLD

PqsH (SEQ ID NO:13)

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PqsL (SEQ ID NO:14)

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 QVRLNDGRVLRPRVVVGADGIASYVRRLLDIDVERRPYSPMLVGTALAPCVAERNRLYVDSQGGLAYF
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***pqsA-E* operon promoter (including ATG start site of *pqsA*) (SEQ ID NO:15)**

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 ACTTTTCTGTTGCGACTCCGAATATCGCGCTTGCACGCGCGCTAGTTTCCCGTTCTGACAAAGCAAG
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***mvfR* (SEQ ID NO:16)**

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 CGCAGCCTGTGAACTACCAGCAGCTGATCGGCGACATCGCCTTCAATCTCAACAAGGTCGCGCAATCT

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AGTAG

MvIR ((SEQ ID NO:17))

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LESARQLRELGRQRFDDAPAWQPSIVETAQRSGPKALAYRQRAAPE

Figure 11

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(% of PA14)	<i>mvfR</i>	<i>phnAB</i>	<i>pqsA</i>	<i>pqsB</i>	<i>pqsE</i>	<i>mvfR</i> compl.	<i>lasR</i>
HHQ	0	48 ± 5	0	0	49 ± 4	1017 ± 247	250 ± 11
HHQ <i>N</i> -oxide	0	110 ± 17	0	0	148 ± 29	200 ± 41	45 ± 8
PQS	0	76 ± 11	0	0	90 ± 13	247 ± 65	23 ± 3
HNQ	0	68 ± 5	0	0	84 ± 5	502 ± 106	551 ± 262
HNQ <i>N</i> -oxide	0	91 ± 15	0	0	135 ± 20	286 ± 52	41 ± 3
diHNQ	0	128 ± 21	0	0	160 ± 27	156 ± 49	19 ± 3
AA	0	90 ± 51	458 ± 221	188 ± 102	24 ± 17	0	6 ± 1
Pyocyanin	<10	24 ± 3	<10	<10	<10	177 ± 26	NT

FIGURE 12

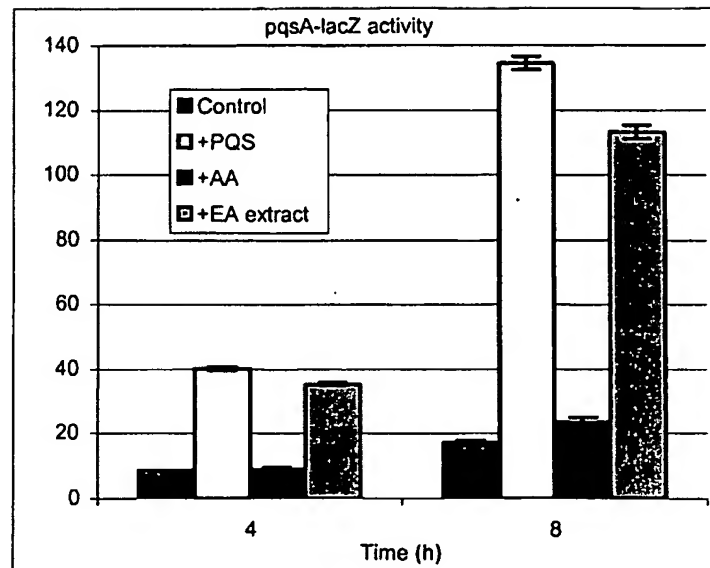
FIGURE 13

	PQS ($\mu\text{g/ml}$)	β -gal activity (MU) [†]
<i>lasR</i> ⁻	2.1 ± 0.1	63.6 ± 2.6
<i>lasR</i> ⁻ + <i>mvfR</i> ⁻	5.2 ± 1.8	110.5 ± 4.3
Ratio [*]	5.0 ± 1.8	3.5 ± 0.2

FIGURE 14

	β -gal activity (MU) [†]	
	PA14	<i>lasR</i> [†]
-HHQ	371 ± 8	78.7 ± 1.5
+HHQ	473 ± 23	83.7 ± 0.2

FIGURE 15



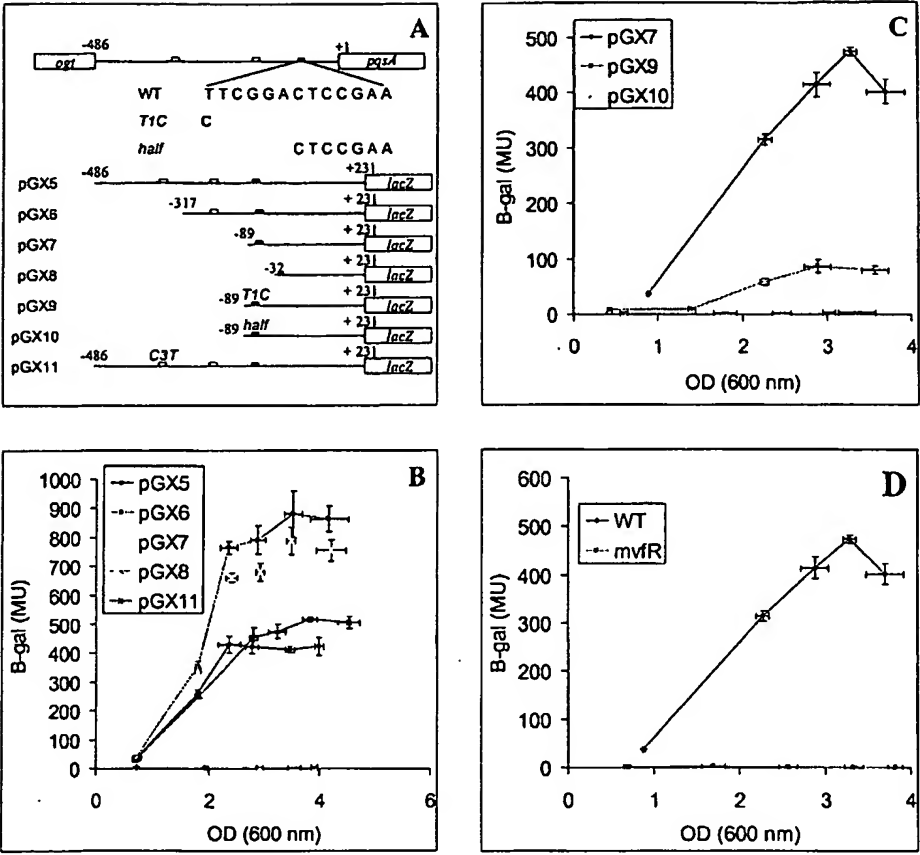


Figure 16